# BIO392-cnv-freq

#### kim wild

#### Step 1: Install package

```
if (!require(devtools)){install.packages("devtools")}

## Loading required package: devtools

## Loading required package: usethis

if (!require(pgxRpi)){devtools::install_github("progenetix/pgxRpi")}

## Loading required package: pgxRpi

library(pgxRpi)
```

#### Step2: Search esophageal adenocarcinoma NCIt code

# Step3: Access the CNV frequency data from samples with esophageal adenocarcinoma

```
freq <- pgxLoader(type = "frequency", output = "pgxseg", filters = "NCIT:C9245", codematches = T)</pre>
```

The retreived data is an object containing two slots meta and data.

The meta slot looks like this:

#### freq\$meta

```
## code label sample_count
## 1 NCIT:C9245 Invasive Breast Carcinoma 3796
## 2 total 3796
```

The data slot includes two matrices.

#### names(freq\$data)

```
## [1] "NCIT:C9245" "total"
```

The frequency matrix looks like this

#### head(freq\$data\$"NCIT:C9245")

##		filters	reference_name	start	end	<pre>gain_frequency</pre>	loss_frequency	no
##	1	NCIT:C9245	1	0	400000	3.556	1.923	1
##	2	NCIT:C9245	1	400000	1400000	4.531	8.667	2
##	3	NCIT:C9245	1	1400000	2400000	2.792	7.719	3
##	4	NCIT:C9245	1	2400000	3400000	5.269	35.643	4
##	5	NCIT:C9245	1	3400000	4400000	4.373	34.905	5
##	6	NCIT:C9245	1	4400000	5400000	4.426	36.170	6

#### Dimension of this matrix

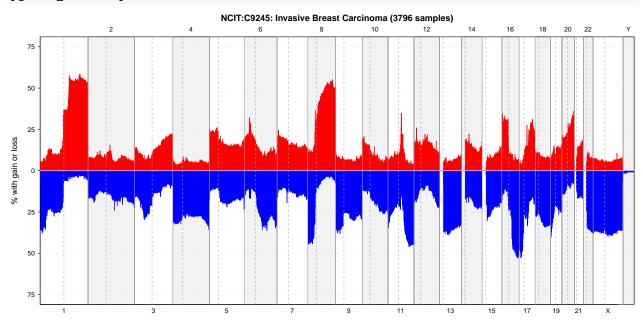
## dim(freq\$data\$"NCIT:C9245")

## [1] 3106 7

## Step4: Visualize data

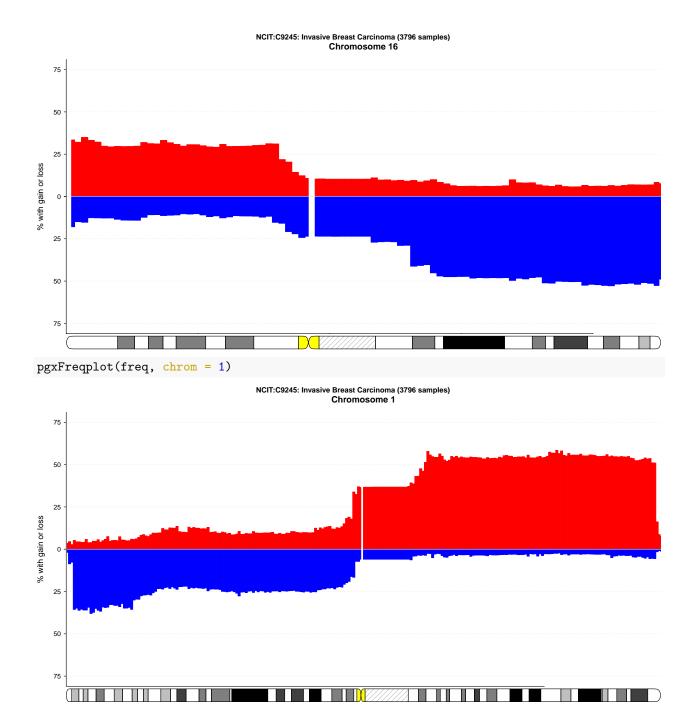
## By genome

## pgxFreqplot(freq)



## By chromosome

pgxFreqplot(freq, chrom = 16)



## Step5: Analyse the data

According the plot, we can see frequenct gains on chromosome 1p, 8p, 16q, 20p and frequenct losses on chromosome 1p, 8p, 11q, 13p, 16p and X both.

But on chr 16 more losses than gains. Chr 1q and 8q have many gains.